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1646

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/525,998

DATE: 10/30/2001

TIME: 15:13:20

Input Set : A:\98385Eseq.txt

Output Set: N:\CRF3\10302001\I525998.raw

3 <110> APPLICANT: Hauptmann, Rudolph
4 Himmeler, Adolph
5 Maurer-Fogy, Ingrid
6 Stratowa, Christian
8 <120> TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
9 Them
11 <130> FILE REFERENCE: 98,385-E
13 <140> CURRENT APPLICATION NUMBER: 09/525,998
14 <141> CURRENT FILING DATE: 2000-03-15
16 <150> PRIOR APPLICATION NUMBER: 08/383,676
17 <151> PRIOR FILING DATE: 1995-02-01
19 <150> PRIOR APPLICATION NUMBER: 08/153,287
20 <151> PRIOR FILING DATE: 1993-11-17
22 <150> PRIOR APPLICATION NUMBER: 07/821,750
23 <151> PRIOR FILING DATE: 1992-01-02
25 <150> PRIOR APPLICATION NUMBER: 07/511,430
26 <151> PRIOR FILING DATE: 1990-04-20
28 <160> NUMBER OF SEQ ID NOS: 87
30 <170> SOFTWARE: PatentIn Ver. 2.0
32 <210> SEQ ID NO: 1
33 <211> LENGTH: 1368
34 <212> TYPE: DNA
35 <213> ORGANISM: Homo sapiens
37 <220> FEATURE:
38 <221> NAME/KEY: CDS
39 <222> LOCATION: (1)..(1368)
41 <220> FEATURE:
42 <221> NAME/KEY: sig_peptide
43 <222> LOCATION: (1)..(87)
45 <220> FEATURE:
46 <221> NAME/KEY: misc_feature
47 <222> LOCATION: (88)..(120)
48 <223> OTHER INFORMATION: Portion of TNF-BP pro protein cleaved by
49 extracellular proteases following secretion.
51 <220> FEATURE:
52 <221> NAME/KEY: misc_feature
53 <222> LOCATION: (606)..(633)
54 <223> OTHER INFORMATION: Portion of TNF-BP pro protein cleaved by
55 extracellular proteases following secretion.
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59 Met Gly Leu Ser Thr Val Pro Asp Leu Leu Pro Leu Val Leu Leu
60 1 5 10 15
62 gag ctg ttg gtg gga ata tac ccc tca ggg gtt att gga ctg gtc cct 96
63 Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro
64 20 25 30
66 cac cta ggg gac agg gag aag aga gat agt gtg tgt ccc caa gga aaa 144

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67 His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys
68      35      40      45
70 tat atc cac cct caa aat aat tcg att tgc tgt acc aag tgc cac aaa 192
71 Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys
72      50      55      60
74 gga acc tac ttg tac aat gac tgt cca ggc ccg ggg cag gat acg gac 240
75 Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp
76 65      70      75      80
78 tgc agg gag tgt gag agc ggc tcc ttc acc gct tca gaa aac cac ctc 288
79 Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu
80      85      90      95
82 aga cac tgc ctc agc tgc tcc aaa tgc cga aag gaa atg ggt cag gtg 336
83 Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val
84      100      105      110
86 gag atc tct tct tgc aca gtg gac cgg gac acc gtg tgt ggc tgc agg 384
87 Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg
88      115      120      125
90 aag aac cag tac cgg cat tat tgg agt gaa aac ctt ttc cag tgc ttc 432
91 Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe
92      130      135      140
94 aat tgc agc ctc tgc ctc aat ggg acc gtg cac ctc tcc tgc cag gag 480
95 Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu
96 145      150      155      160
98 aaa cag aac acc gtg tgc acc tgc cat gca ggt ttc ttt cta aga gaa 528
99 Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu
100      165      170      175
102 aac gag tgt gtc tcc tgt agt aac tgt aag aaa agc ctg gag tgc acg 576
103 Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr
104      180      185      190
106 aag ttg tgc cta ccc cag att gag aat gtt aag ggc act gag gac tca 624
107 Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser
108      195      200      205
110 ggc acc aca gtg ctg ttg ccc ctg gtc att ttc ttt ggt ctt tgc ctt 672
111 Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu
112      210      215      220
114 tta tcc ctc ctc ttc att ggt tta atg tat cgc tac caa cgg tgg aag 720
115 Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys
116 225      230      235      240
118 tcc aag ctc tac tcc att gtt tgt ggg aaa tcg aca cct gaa aaa gag 768
119 Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu
120      245      250      255
122 ggg gag ctt gaa gga act act act aag ccc ctg gcc cca aac cca agc 816
123 Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser
124      260      265      270
126 ttc agt ccc act cca ggc ttc acc ccc acc ctg ggc ttc agt ccc gtg 864
127 Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val
128      275      280      285
130 ccc agt tcc acc ttc acc tcc agc tcc acc tat acc ccc ggt gac tgt 912
131 Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys

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132      290      295      300
134 ccc aac ttt gcg gct ccc cgc aga gag gtg gca cca ccc tat cag ggg 960
135 Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly
136 305      310      315      320
138 gct gac ccc atc ctt gcg aca gcc ctc gcc tcc gac ccc atc ccc aac 1008
139 Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn
140      325      330      335
142 ccc ctt cag aag tgg gag gac agc gcc cac aag cca cag agc cta gag 1056
143 Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp
144      340      345      350
146 act gat gac ccc gcg acg ctg tac gcc gtg gtg gag aac gtg ccc ccg 1104
147 Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro
148      355      360      365
150 ttg cgc tgg aag gaa ttc gtg cgg cgc cta ggg ctg agc gac cac gag 1152
151 Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu
152      370      375      380
154 atc gat cgg ctg gag ctg cag aac ggg cgc tgc ctg cgc gag gcg caa 1200
155 Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln
156 385      390      395      400
158 tac agc atg ctg gcg acc tgg agg cgg cgc acg ccg cgg cgc gag gcc 1248
159 Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala
160      405      410      415
162 acg ctg gag ctg ctg gga cgc gtg ctc cgc gac atg gac ctg ctg ggc 1296
163 Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly
164      420      425      430
166 tgc ctg gag gac atc gag gag gcg ctt tgc ggc ccc gcc gcc ctc ccg 1344
167 Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro
168      435      440      445
170 ccc gcg ccc agt ctt ctc aga tga 1368
171 Pro Ala Pro Ser Leu Leu Arg
172      450      455
175 <210> SEQ ID NO: 2
176 <211> LENGTH: 455
177 <212> TYPE: PRT
178 <213> ORGANISM: Homo sapiens
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182 1 5 10 15
184 Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro
185 20 25 30
187 His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys
188 35 40 45
190 Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys
191 50 55 60
193 Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp
194 65 70 75 80
196 Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu
197 85 90 95
199 Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val

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200          100          105          110
202 Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg
203          115          120          125
205 Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe
206          130          135          140
208 Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu
209 145          150          155          160
211 Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu
212          165          170          175
214 Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr
215          180          185          190
217 Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser
218          195          200          205
220 Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu
221          210          215          220
223 Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys
224 225          230          235          240
226 Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu
227          245          250          255
229 Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser
230          260          265          270
232 Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val
233          275          280          285
235 Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys
236          290          295          300
238 Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly
239 305          310          315          320
241 Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn
242          325          330          335
244 Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp
245          340          345          350
247 Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro
248          355          360          365
250 Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu
251          370          375          380
253 Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln
254 385          390          395          400
256 Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala
257          405          410          415
259 Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly
260          420          425          430
262 Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro
263          435          440          445
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266          450          455
269 <210> SEQ ID NO: 3
270 <211> LENGTH: 483
271 <212> TYPE: DNA
272 <213> ORGANISM: Homo sapiens

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274 <220> FEATURE:

275 <221> NAME/KEY: CDS

276 <222> LOCATION: (1)..(483)

278 <400> SEQUENCE: 3

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281 1 5 10 15
283 att tgc tgt acc aag tgc cac aaa gga acc tac ttg tac aat gac tgt 96
284 Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys
285 20 25 30
287 cca ggc ccg ggg cag gat acg gac tgc agg gag tgt gag agc ggc tcc 144
288 Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser
289 35 40 45
291 ttc acc gct tca gaa aac cac ctc aga cac tgc ctc agc tgc tcc aaa 192
292 Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys
293 50 55 60
295 tgc cga aag gaa atg ggt cag gtg gag atc tct tct tgc aca gtg gac 240
296 Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp
297 65 70 75 80
299 cgg gac acc gtg tgt ggc tgc agg aag aac cag tac cgg cat tat tgg 288
300 Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp
301 85 90 95
303 agt gaa aac ctt ttc cag tgc ttc aat tgc agc ctc tgc ctc aat ggg 336
304 Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly
305 100 105 110
307 acc gtg cac ctc tcc tgc cag gag aaa cag aac acc gtg tgc acc tgc 384
308 Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys
309 115 120 125
311 cat gca ggt ttc ttt cta aga gaa aac gag tgt gtc tcc tgt agt aac 432
312 His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser Asn
313 130 135 140
315 tgt aag aaa agc ctg gag tgc acg aag ttg tgc cta ccc cag att gag 480
316 Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu
317 145 150 155 160
319 aat 483
320 Asn

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323 <210> SEQ ID NO: 4

324 <211> LENGTH: 161

325 <212> TYPE: PRT

326 <213> ORGANISM: Homo sapiens

328 <400> SEQUENCE: 4

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329 Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser
330 1 5 10 15
332 Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys
333 20 25 30
335 Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser
336 35 40 45
338 Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys
339 50 55 60

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Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

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Input Set : A:\98385Eseq.txt

Output Set: N:\CRF3\10302001\I525998.raw

L:684 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:812 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:844 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:882 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1416 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:1436 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:1482 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:1548 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:1623 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31
L:1664 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33
L:1667 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33
L:1686 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34
L:1689 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34
L:1722 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36

*Pat in 20
Mr. Z...*